



Replacement Sheet

Figure 3A

Clustal W(1.4) multiple sequence alignment

7 Sequences Aligned. Alignment Score = 118839
Gaps Inserted = 0 Conserved Identities = 936

Pairwise Alignment Mode: Fast
Pairwise Alignment Parameters:
ktup = 1 Gap Penalty = 3 Top Diagonals = 5 Window Size = 5

Multiple Alignment Parameters:
Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1
Delay Divergent = 40% Gap Distance = 8
Similarity Matrix: blosum

Processing time: 12.9 seconds

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Spy74_M3      1                               DYAES      5
Spy70_M5      1          LVKEPILKQTQASSSISGADYAES    24
Spy69_M6      1                               KQTQASSSISGADYAES    17
Spy68_M2      1          LVKEPILKQTQASSSISGADYAES    24
Spy60_M1      1          LVKEPILKQTQASSSISGADYAES    24
12357_M18     1          VKEPILKQTQASSSISGADYAES    23
700294_M1     1  MKKHLKTVALTLTTVSVVTHNQEVFSLVKEPILKQTQASSSISGADYAES    50
                                     *****

Spy74_M3      6  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    55
Spy70_M5     25  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    74
Spy69_M6     18  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    67
Spy68_M2     25  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    74
Spy60_M1     25  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    74
12357_M18    24  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    73
700294_M1    51  SGKSKLKINETSGPVDDTVTDLFSDKRRTTPEKIKDNLAKGPREQELKAVT    100
                *****

Spy74_M3     56  ENTESEKQITSGSQLEQSKESLSLNKRVSTSNWEICDFITKGNTLVGLS    105
Spy70_M5     75  ENTESEKQINSGSQLEQSKESLSLNKRVSTSNWEICDFITKGNTLVGLS    124
Spy69_M6     68  ENTESEKQINSGSQLEQSKESLSLNKRVSTSNWEICDFITKGNTLVGLS    117
Spy68_M2     75  ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS    124
Spy60_M1     75  ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS    124
12357_M18    74  ENTESEKQINSGSQLEQSKESLSLNKRVSTSNWEICDFITKGNTLVGLS    123
700294_M1   101  ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS    150
                *****

Spy74_M3     106 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    155
Spy70_M5     125 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
Spy69_M6     118 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    167
Spy68_M2     125 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
Spy60_M1     125 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    174
12357_M18    124 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    173
700294_M1    151 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE    200
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Figure 3B

Spy74_M3	156	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	205
Spy70_M5	175	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy69_M6	168	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	217
Spy68_M2	175	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy60_M1	175	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
12357_M18	174	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	223
700294_M1	201	NGEISQLDVDGKEI INEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	250

Spy74_M3	206	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	255
Spy70_M5	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
Spy69_M6	218	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	267
Spy68_M2	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
Spy60_M1	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
12357_M18	224	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	273
700294_M1	251	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	300

Spy74_M3	256	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	305
Spy70_M5	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy69_M6	268	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	317
Spy68_M2	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy60_M1	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
12357_M18	274	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	323
700294_M1	301	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	350

Spy74_M3	306	IESEAFNGPNPDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	355
Spy70_M5	325	IESEAFNGPNPDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy69_M6	318	IESEAFNGPNPDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	367
Spy68_M2	325	IESEAFNGPNPDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy60_M1	325	IESEAFNGPNPDDHYNNRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP	374
12357_M18	324	IESEAFNGPNPDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	373
700294_M1	351	IESEAFNGPNPDDHYNNRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP	400

Spy74_M3	356	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	405
Spy70_M5	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	424
Spy69_M6	368	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	417
Spy68_M2	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	424
Spy60_M1	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	424
12357_M18	374	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	423
700294_M1	401	EIDYTKWLEEDFTYQKNSVTGFSSKGLQVKRNKNLEIPKQHNGVTITEI	450

Spy74_M3	406	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	455
Spy70_M5	425	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
Spy69_M6	418	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	467
Spy68_M2	425	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
Spy60_M1	425	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
12357_M18	424	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	473
700294_M1	451	GDNAFRNVDFQNKTLRKYLDEEVKLPSTIRKIGAFQSNNLKSFEASDD	500

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Figure 3C

Spy74_M3	456	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	505
Spy70_M5	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
Spy69_M6	468	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	517
Spy68_M2	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
Spy60_M1	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
12357_M18	474	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	523
700294_M1	501	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	550

Spy74_M3	506	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	555
Spy70_M5	525	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy69_M6	518	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	567
Spy68_M2	525	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy60_M1	525	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
12357_M18	524	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	573
700294_M1	551	SAFRQNGANNLI FMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	600

Spy74_M3	556	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	605
Spy70_M5	575	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	624
Spy69_M6	568	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	617
Spy68_M2	575	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	624
Spy60_M1	575	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	624
12357_M18	574	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	623
700294_M1	601	SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALS HIAFNALDDNDGD	650

Spy74_M3	606	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILK LIEGLDY	655
Spy70_M5	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	674
Spy69_M6	618	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	667
Spy68_M2	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMIDLEKILK LIEGLDY	674
Spy60_M1	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	674
12357_M18	624	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	673
700294_M1	651	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILK LIEGLDY	700

Spy74_M3	656	STLRQTTQTQFRDMTTAGKALLSKSKLRQGEKQKFLQEAQFFLGRVDLDK	705
Spy70_M5	675	STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK	724
Spy69_M6	668	STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK	717
Spy68_M2	675	STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK	724
Spy60_M1	675	STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK	724
12357_M18	674	STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK	723
700294_M1	701	STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK	750

Spy74_M3	706	AIAKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	755
Spy70_M5	725	AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy69_M6	718	AIAKAEKALVTKKATKNGQLLERSINKAVSAYNNSAIKKANVKRLEKELD	767
Spy68_M2	725	AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy60_M1	725	AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD	774
12357_M18	724	AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD	773
700294_M1	751	AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD	800

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Figure 3D

Spy74_M3	756	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	805
Spy70_M5	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
Spy69_M6	768	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	817
Spy68_M2	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
Spy60_M1	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
12357_M18	774	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	823
700294_M1	801	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	850

Spy74_M3	806	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	855
Spy70_M5	825	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	874
Spy69_M6	818	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	867
Spy68_M2	825	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	874
Spy60_M1	825	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	874
12357_M18	824	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	873
700294_M1	851	LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN	900

Spy74_M3	856	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	905
Spy70_M5	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKAGTHSEKSSSS	924
Spy69_M6	868	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	917
Spy68_M2	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGMHSEKSSSS	924
Spy60_M1	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	924
12357_M18	874	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	923
700294_M1	901	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEEAEQLLPKPGTHSEKSSSS	950
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Spy74_M3	906	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	951
Spy70_M5	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	970
Spy69_M6	918	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	963
Spy68_M2	925	ESANSKDRGLQSHPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL	971
Spy60_M1	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL	971
12357_M18	924	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	969
700294_M1	951	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALLSLI	1000

Spy74_M3	952	951
Spy70_M5	971	970
Spy69_M6	964	963
Spy68_M2	972	971
Spy60_M1	972	971
12357_M18	970	969
700294_M1	1001	TAIKKKKY 1008